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10/549,262	05/10/2006	Petra Peters-Wendisch	23369	5108

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EXAMINER	
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1652	

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Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary	Application No.	Applicant(s)	
	10/549,262	PETERS-WENDISCH ET AL.	
	Examiner	Art Unit	
	MD. YOUNUS MEAH	1652	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE ____ MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☐ Responsive to communication(s) filed on _____.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☐ Claim(s) _____ is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☐ Claim(s) _____ is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☐ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

Claims 1-8 and 14-20 were examined in the previous action. With supplemental amendment of this application, the applicant, on dates 2/20/08, cancelled claims 9-13, 21-25, amended claims 1, 14-15, 17 and added new claims 26- 28. Claims 1-8, 14-20, 26-28 are examined here.

Claim Objection

Claims 1,-3, 14-15, 20, 26, 28 are objected to as being written in such poor English that the claims are barely understandable. Appropriate correction is required.

Claim Rejection

35 U.S.C 112

Claims 1-6, 14-15, 17-20, 26-28 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claims 1,-3, 14-15, 20, 26, 28 are indefinite because these claims are generally narrative and indefinite, failing to conform with current U.S. practice. They appear to be a literal translation into English from a foreign document and are replete with grammatical and idiomatic errors.

Claims 1, (2-6, 14-15, 17-20 and 28 dependent on claim 1) are indefinite as the recitation of "fragments of the nucleotide sequence according to SEQ ID NO 1 encoding L-serine dehydratase flanking the 5' end and the 3' end of said nucleotide sequence

encoding L-serine dehydratase to permit complete removal of said nucleotide sequence encoding L-serine dehydratase by homologous recombination" make the claim confusing. It is unclear how fragments of SEQ ID NO: 1 permit complete removal of "said nucleotide sequence encoding L-serine dehydratase".

Claim 3 is indefinite in recitation of "homolog", as it is unclear how similar to SEQ ID NO: 1 a "homolog" must be. Applicants' argument that homolog is complementary to SEQ ID NO: 1 still make it unclear because a homolog complementary to SEQ ID NO: 1 reads on undefined fragments of SEQ ID NO: 1.

Claim 3 is indefinite in recitation of "allele functionally equivalent", as it is unclear how similar to SEQ ID NO: 1 an "allele functionally equivalent" is.

Claim 3 is indefinite in the recitation of "stringent conditions" as the specification does not define what conditions constitute "stringent". While page 11 of the specification describes some conditions, which are intended to be stringent, there is nothing to suggest that other conditions would not also be included within the scope of this term and in the art what is considered stringent varies widely depending on the individual situation as well as the person making the determination. As such it is unclear how homologous to the sequence of a gene of SEQ ID NO: 1, a sequence must be to be included within the scope of these claims.

Claim 14 the recitation "an endogenous nucleotide sequence which encodes an L-serine dehydratase, which is deleted in whole or in part or is mutated and which is expressed to a reduced extent in comparison with expression of the naturally occurring L-serine dehydratase having nucleotide sequence of SEQ ID NO: 1 or is not expressed

at all, so that the endogenous nucleotide sequence encoding L-serine dehydratase no longer encodes a protein with L- serine dehydratase activity" makes the claim unclear as the phrase "so that the endogenous nucleotide sequence encoding L-serine dehydratase no longer encodes a protein with L- serine dehydratase activity" makes no sense. Does it encode any protein and if it does what protein? It is suggested that the claim recite "an endogenous nucleotide sequence which encodes an L-serine dehydratase, which is modified by deletion or mutation wherein the modified sequence does not encode a protein with L-serine dehydratase activity"

Claims 4-6 are confusing in the recitation of " isolated from a coryneform bacteria" as the nucleic acids recited in claim 1 are not naturally occurring nucleic acids

Claim 20 the recitation a probe for " isolating" makes the claim unclear as it is not clear how a probe can isolate a gene.

35 U.S.C. 112 first paragraph Written description:

Rejection of Claims 1-8, 14-20 under 112 1st paragraph written description is maintained as explained in the previous office action and explained below: (:

Claims 1-8, 14-20 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. These claims are directed to any DNA construct comprising any serA, serB and serC gene and any

Comment [e1]: I don't think we can withdrawn all WD rejections except with regard to the scope of serA, serB and serC genes. There are still issues in the claims to modified microorganisms and constructs for their construction with regard to the identifying characteristics of the microorganisms/genes to be modified and structure of the constructs for modification. Also issues regarding the structure of the probes recited in claim 20

mutant version of a serine dehydratase (sdaA) gene of SEQ ID NO: 1 or a homologue or variant thereof which is capable of homologous recombination with an endogenous serine dehydratase gene of any microorganism to produce a microorganism having reduced serine dehydratase activity or any fragment of 10-30 nucleotides SEQ ID NO: 1 and any microorganism comprising said DNA construct. The specification teaches the structure of only a single representative species of such DNA serine dehydratase (mutated SEQ ID NO: 1 wherein one or more residues from position 506-918 of SEQ ID NO is deleted) and a DNA construct comprising said sdaA with a few serA, serB and serC genes. Moreover, the specification fails to describe any other representative species by any identifying characteristics or properties other than having reduced/not having l-serine dehydratase activity. Given this lack of description of representative species encompassed by the genus of the claim, the specification fails to sufficiently describe the claimed invention in such full, clear, concise, and exact terms that a skilled artisan would recognize that applicants were in possession of the claimed invention.

Claims 1-8, 14-20 and 26-28 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. These claims are directed to a genus of nucleic acids encoding genus of serA, serB and serC genes having any structure. The specification teaches the structure of only a single representative species of such DNAs (in plasmid pEC-T18mob2-srA^{fbr}CB) The

specification does not contain any disclosure of the structure of all nucleic acid sequences included in the claimed genera. The genus of nucleic acids claimed is a large variable genus with the potentiality of encoding many different proteins. Therefore, many structurally distinct nucleic acids are encompassed within the scope of these claims. A sufficient written description of a genus of DNAs may be achieved by a recitation of a representative number of DNAs defined by nucleotide sequence or a recitation of structural features common to members of the genus, **which features constitute a substantial portion of the genus.**

Applicants' are referred to the revised guidelines concerning compliance with the written description requirement of U.S.C. 112, first paragraph, published in the Official Gazette and also available at www.uspto.gov.

Applicants' arguments against rejection of claims 1-8, 14-20 under 35 U.S.C. 112, first paragraph written description are acknowledged but not found persuasive. Applicants in their amendment at page 11-12 argue that their polynucleotide expresses at least one serine biosynthesis sequence (serA, serB or serC) is the polynucleotide sequence that is needed to catalyze the conversion of a carbohydrate, such as glucose, to L-serine. The polynucleotide sequence L-serine dehydratase, which is also present as part of the recombinant nucleic acid for promoting microbial production of L- serine from the carbohydrates, because the expressed enzyme L-serine dehydratase facilitates the degradation of L-serine to pyruvate. Thus it is desirable to limit as much as possible the expression of the portion of the polynucleotide sequence that expresses L-serine dehydratase to prevent the undesired degradation of the L-serine dehydratase.

The specification on page 6, line 11 through page 11, and line 15 adequately defines the presently claimed recombinant nucleic acids, and adequately discloses how to make and how to use the presently claimed recombinant nucleic acids.

However recited claims comprise any ser biosynthetic gene having any structure. Polynucleotide expressing any serine biosynthesis sequence comprising any serA, serB or serC having no structural limitation from any source comprise any polynucleotide from a vast number of genes encoding any protein (including any number of mutation, substitution, addition to any protein sequence) that shows serine synthase activity. Specification, as explained above, does not teach all these variant of serine biosynthetic genes. Therefore one of skill in the art would not recognize from the disclosure that applicants' were in possession of the claimed invention.

35 U.S.C. 112 first paragraph Enablement:

Claims 1-8, 14-20 and 26-27 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for the DNA molecule (plasmid pK19mobsacB-□sdaA or plasmid pEC-T18mob2-srA^{fbr}CB comprising specific ser enzyme and mutated DNA of SEQ ID NO: 1 wherein residues 506-918 are mutated so that said DNA shows no or reduced sdaA activity compared to unmutated SEQ ID NO: 1, any transformed bacteria incorporating the said plasmid , does not reasonably provide enablement for any DNA or any fragment thereof or DNA molecule that hybridize with any mutant of SEQ ID NO:1 or any homolog or allelic variant thereof or

any probe comprising 10-30 nucleic acid of SEQ ID NO: 1 or any nucleic acids encoding any serA, serB and serC having any structure and vector and bacteria incorporated by the said DNA. Claims 14-15, and 17-19 while being enabling for the microorganism which endogenous serine dehydratase gene of SEQ ID NO: 1 has been deleted or residues 506-918 are mutated and which expresses plasmid pK19mobsacB or plasmid pEC-T18mob2-srA^{fbr}CB. does not enable for any microorganism comprising any serA, serB or serC gene and in which any endogenous serine dehydratase gene has been deleted or mutated such that the microorganism has reduced serine dehydratase activity. Microorganism recited in these claims comprise any microorganism from any source comprise unlimited number of species. One knowledgeable in prior art need to perform infinite number of experimentation to find out which microorganism is comprise ser biosynthetic enzyme and sdaA and how to delete or mutate said sdaA. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the invention commensurate in scope with these claims. Claims 3 and 20 are rejected under 35 U.S.C. 112, first paragraph, because the specification does not reasonably provide enablement for any allelic variant or nucleic acid comprising a fragment of 10-30 nucleotides SEQ ID NO: 1. An allelic variant can have any number of variations. or a fragment comprising 10-30 nucleotides SEQ ID NO: 1 can have any number of variations therefrom and can be as short as 10 nucleotides encompassed within any amount of additional variation of SEQ ID NO: 1. The scope of the claims is not commensurate with the enablement provided by the disclosure with regard to the

extremely large number of nucleic acids encompassed. The disclosed use for the claimed nucleic acids is as probes within a diagnostic procedure to determine the presence of absence of particular sdaA variants. However only fragments of the sdaA gene which are 100% identical to a portion of a particular sdaA allele would be suitable probes for distinguishing the presence or absence of that allele as nucleic acids with other variations or embedded within substantial amounts of additional sequence would not hybridize to distinct alleles differentially. Since the nucleotide sequence of a probe determines its structural and functional properties, predictability of which variants of a known sequence can be used as a probe for a given target sequence requires a knowledge of and guidance with regard to the ways in which the probes' structure relates to the desired function. However, in this case the disclosure is limited to the nucleic acid of SEQ ID NO: 1.

Claims 1-8, 26-27 are so broad as to encompass any DNA construct comprising any serA, serB and serC gene and any mutant version of a serine dehydratase gene of SEQ ID NO: 1 or a homologue or variant thereof which is capable of homologous recombination with an endogenous serine dehydratase gene of any microorganism to produce a microorganism having reduced serine dehydratase activity. and vector and bacteria comprising said DNA construct. Claims 14-19 are so broad as to encompass any microorganism comprising any serA, serB or serC gene and in which any endogenous serine dehydratase gene has been deleted or mutated such that the microorganism has reduced serine dehydratase activity . The scope of the claims is not commensurate with the enablement provided by the disclosure with regard to the

Comment [e2]: I have written this for you to try and help you see what I am looking for in this case since all previous attempts to get you to reword the descriptions of what these claims presumably encompass seem to have gotten nowhere. These are not just classic gene encoding a protein to be expressed claims and trying to write a description of them in these terms just doesn't work. I want you to similarly revise the remainder of the rejection to try and address the scope issues that are relevant here particularly with regard to the scope of microorganisms which are to be modified and the scope of the structural characteristics of the constructs which are necessary for successful use in homologous recombination. The standard FP is really only relevant to the features of the serA, serB and serC gene which must be present and you will likely simply need to write your own discussion for the other issues.

extremely large number DNAs and microorganisms broadly encompassed by the claims. Since the amino acid sequence of a protein determines its structural and functional properties, predictability of which changes can be tolerated in a protein's amino acid sequence and obtain the desired activity requires a knowledge of and guidance with regard to which amino acids in the protein's sequence, if any, are tolerant of modification and which are conserved (i.e. expectedly intolerant to modification), and detailed knowledge of the ways in which the proteins' structure relates to its function. However, in this case the disclosure is limited to the DNA expressed in plasmid pEC-T18mob2-srA^{fbr}CB comprising mutation of residues 506-918 nucleotide of SEQ ID NO: 1 encoding a protein having reduced sdaA activity.

While recombinant and mutagenesis techniques are known, it is not routine in the art to screen for multiple substitutions or multiple modifications, as encompassed by the instant claims, and the positions within a protein's sequence where amino acid modifications can be made with a reasonable expectation of success in obtaining the desired activity/utility are limited in any protein and the result of such modifications is unpredictable. In addition, one skilled in the art would expect any tolerance to modification for a given protein to diminish with each further and additional modification, e.g. multiple substitutions.

The specification does not support the broad scope of the claims, which encompass any DNA construct comprising any serA, serB and serC gene and any mutant version of a serine dehydratase gene of SEQ ID NO:1 or a homologue or variant thereof which is capable of homologous recombination with an endogenous serine

dehydratase gene of any microorganism to produce a microorganism having reduced serine dehydratase activity, microorganism comprising said DNA construct because the specification does **not** establish: (A) regions of the protein structure which may be modified to eliminate or reduce sdaA and effect serA, serB and serC activity; (B) the general tolerance of sdaA, serA, serB and serC gene to modification and extent of such tolerance; (C) a rational and predictable scheme for modifying any sdaA , serA, serB and serC nucleotide residues with an expectation of obtaining the desired biological function; and (D) the specification provides insufficient guidance as to which of the essentially infinite possible choices is likely to be successful.

Thus, applicants have not provided sufficient guidance to enable one of ordinary skill in the art to make and use the claimed invention in a manner reasonably correlated with the scope of the claims broadly including any DNA construct comprising any serA, serB and serC gene and any mutant version of a serine dehydratase gene of SEQ ID NO:1 or a homologue or variant thereof which is capable of homologous recombination with an endogenous serine dehydratase gene of any microorganism to produce a microorganism having reduced serine dehydratase activity, microorganism comprising said DNA construct . The scope of the claims must bear a reasonable correlation with the scope of enablement (In re Fisher, 166 USPQ 19 24 (CCPA 1970)). Without sufficient guidance, determination of sdaA genes, having the desired biological characteristics is unpredictable and the experimentation left to those skilled in the art is

unnecessarily, and improperly, extensive and undue. See In re Wands 858 F.2d 731, 8 USPQ2nd 1400 (Fed. Cir, 1988).

Applicants' arguments against rejection of claims 1-8 and 14-20 under 35 U.S.C. 112, first paragraph enablement requirement are acknowledged but not found persuasive as explained above. Applicants in their amendment at page 12 argue that their polynucleotide expresses at least one serine biosynthesis sequence (serA, serB or serC) is the polynucleotide sequence that is needed to catalyze the conversion of a carbohydrate, such as glucose, to L-serine. The polynucleotide sequence L-serine dehydratase, which is also present as part of the recombinant nucleic acid for promoting microbial production of L- serine from the carbohydrates, because the expressed enzyme L-serine dehydratase facilitates the degradation of L-serine to pyruvate. Thus it is desirable to limit as much as possible the expression of the portion of the polynucleotide sequence that expresses L-serine dehydratase to prevent the undesired degradation of the L-serine dehydratase. The specification on page 6, line 11 through page 11, and line 15 adequately defines the presently claimed recombinant nucleic acids, and adequately discloses how to make and how to use the presently claimed recombinant nucleic acids.

However the recited claims comprise any DNA construct comprising any serA, serB and serC gene and any mutant version of a serine dehydratase gene of SEQ ID NO:1 or a homologue or variant thereof which is capable of homologous recombination with an endogenous serine dehydratase gene of any microorganism to produce a microorganism having reduced serine dehydratase activity or any microorganism

comprising said DNA construct. Nucleic acid comprising any nucleic acids encoding any serA, serB and serC having any structure and any mutated fragment of DNA of sdaA of SEQ ID NO: 1 that lack sdaA activity comprise a large variant of genus potentially include many proteins with diverse structures. To find out which microorganism having these large number of DNAs can over produce L-serine one of ordinary skill would be required to conduct enormous number of experimentations. This would clearly constitute **undue** experimentation. While enablement is not precluded by the necessity for routine screening, if a large amount of screening is required, the specification must provide a reasonable amount of guidance with respect to the direction in which the experimentation should proceed. Such guidance has **not** been provided in the instant specification. As previously stated the specification does not establish: (A) regions of the protein structure which may be modified to eliminate or reduce sdaA and affect serA, serB and serC activity; (B) the general tolerance of sdaA, serA, serB and serC gene to modification and extent of such tolerance; (C) a rational and predictable scheme for modifying any sdaA , serA, serB and serC nucleotide residues with an expectation of obtaining the desired biological function; and (D) the specification provides insufficient guidance as to which of the essentially infinite possible choices is likely to be successful.

Comment [e3]: the DNAs do not have serine production activity

CLAIM Rejection - 35 U.S.C 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> (a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent. (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Rejection of claims 1-2, 4-8 and 16 under 35 U.S.C. 102(b) as being anticipated by Kubota et al. (*Agr.Biol. Chem* 1985, vol. 49, pp 7-12, from ids) is withdrawn after amendment of claim 1.

However claims 14-15, 17-19 remain rejected under 35 U.S.C. 102(b) as being anticipated by Kubota et al. (*Agr.Biol. Chem* 1985, vol. 49, pp 7-12,, from ids)

Kubota et al. teach a corynform bacteria having mutated sdaA gene which shows reduced L-serine dehydratase activity and increased production of L-serine. Applicants' argument against Kubata et al is considered but not found persuasive. Applicant argue that KUBOTA et al discloses no structure of the polynucleotide sequence expressing L-serine dehydratase, only discloses undirected mutagenesis methods to increase the production of L-serine and to reduce the activity of the L-serine dehydratase by 32%. However claims 14-15, 17-19 are directed to a microorganism having mutation of naturally occurring L-serine dehydratase gene. Therefore like applicants Kubota et al teach that microorganism having mutated sdaA (naturally occurring L-serine dehydratase) gene shows reduce sdaA activity and also found that said bacteria shows increase production of L-serine.

CLAIM Rejection - 35 U.S.C 103a

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

Claims 1-3, 4-8, 14-20, 26-28 are rejected under 35 U.S.C. 103(a) by Kubota et al. (*Agr.Biol. Chem* 1985, vol. 49, pp 7-12, from ids) in view of Nakagawa et al. (US20020197605)

Kubota et al teach microorganism having mutated sdaA gene shows reduced sdaA activity and shows increased production of L-serine. However, Kobuta does not teach mutation of serine dehydratase of SEQ ID NO: 1.

Nakagawa et al. teaches a gene of SEQ ID NO: 1 of corynebacterium glutamicum which is 100% identical to applicants' serine dehydratase of SEQ ID NO: 1 isolated from corynebacterium glutamicum. Nakagawa et al. also teaches that said gene encodes a serine deaminase (other name of serine dehydratase). Nakagawa et al. gene of SEQ ID NO: 1 encodes same serine dehydatase that applicant teach. L-serine is widely used in food and pharmaceutical industry. In L-serine producing bacteria (such as corynebacterium glutamicum) sdaA degrade L-serine (Kubota et al.).

One knowledgeable of the prior arts (Kobuta et al) is **motivated, to** mutate or delete whole or a portion of the serine dehydratase gene of SEQ ID NO: 1 (sdaA of SEQ ID NO: 1 is taught by Nakagawa et al.) of a *Corynebacterium glutamicum* bacterium so that said bacterium increases the production of L-serine. As such it would have been obvious to one of ordinary skill in the art to mutate (delete the whole gene or a part of gene so that mutant microorganism shows reduced sdaA activity) the gene of SEQ ID NO: 1 of *Corynebacterium glutamicum* as taught by Kobuta et al to reduce sdaA activity and replace the endogenous sdaA gene of a bacterium by mutated sdaA gene of SEQ ID NO: 1 so that said bacterium will produce more L-serine.

Applicants argue that Kobuta et al mutant *Corynebacterium glutamicum* shows only 32% reduction of sdaA activity wherein Kobuta et al perform undirected mutagenesis of sdaA gene of *Corynebacterium glutamicum* and the further argue that finding of reduction of 32% reduction of sdaA activity is accidental. This is not found persuasive. Kobuta et al do teach microorganism having mutated sdaA gene shows reduced sdaA activity and shows increase production of L-serine.

Applicants argue that though Nakagawa et al teach applicants sdaA gene of SEQ ID NO: 1 from *Corynebacterium glutamicum* but it is one of 3009 genes they teach from *Corynebacterium glutamicum* and they identify it serine deaminase (serine dehydratase), Applicants further argue that Nakagawa did not isolate the serine dehydratase gene. They have neither cloned that gene, nor identified its function in an enzyme assay and further argue that it could well be that the gene whose sequence

they inferred from the genome sequence could have a different function than deaminating L-serine, or it could even be that the gene was a pseudogene gene, that means fully inactive, without function. They further argue that, therefore Nakagawa et al teaching has no inventive step. Applicants argument is considered but not found persuasive against using Nakagawa et al in the above 35 U.S.C. 103(a) rejection. Nakagawa gene of SEQ ID NO: 1 of *Corynebacterium glutamicum* is 100% identical to applicant gene of SEQ ID NO: 1 isolated from *Corynebacterium glutamicum*. Nakagawa et al. also teaches that their gene of SEQ ID NO: 1 encodes a serine deaminase (other name of serine dehydratase). It is immaterial whether Nakagawa isolated their gene or not or cloned or not, what matter is that their gene of SEQ ID NO: 1 of *Corynebacterium glutamicum* encode serine deaminase and identical to applicant gene of SEQ ID NO: 1 isolated from *Corynebacterium glutamicum*. Applicants argument that Nakagawa's gene of SEQ ID NO: 1 of *Corynebacterium glutamicum* whose sequence they inferred from the genome sequence which is 100% identical to applicants' gene of SEQ ID NO: 1 isolated from *Corynebacterium glutamicum* could have a different function than deaminating L-serine (serine dehydratase) , or it could even be that the gene was a pseudogene gene, that means fully inactive, without function is not persuasive. Nakagawa et al. gene of SEQ ID NO: 1 is from *Corynebacterium glutamicum* like that of applicants serine dehydratase gene of SEQ ID NO: 1 Therefore Nakagawa et al. gene of SEQ ID NO: 1 and applicants serine dehydratase gene of SEQ ID NO: 1 are the same gene would have same function as they comprise identical structure.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Mohammad Meah whose telephone number is 571-272-1261. The examiner can normally be reached on 8:30-5PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor Nashaat T. Nash can be reached on 571-272-0934. The fax phone number for the organization where this application or proceeding is assigned is571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

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